

FIG. 1



**FIG. 2**

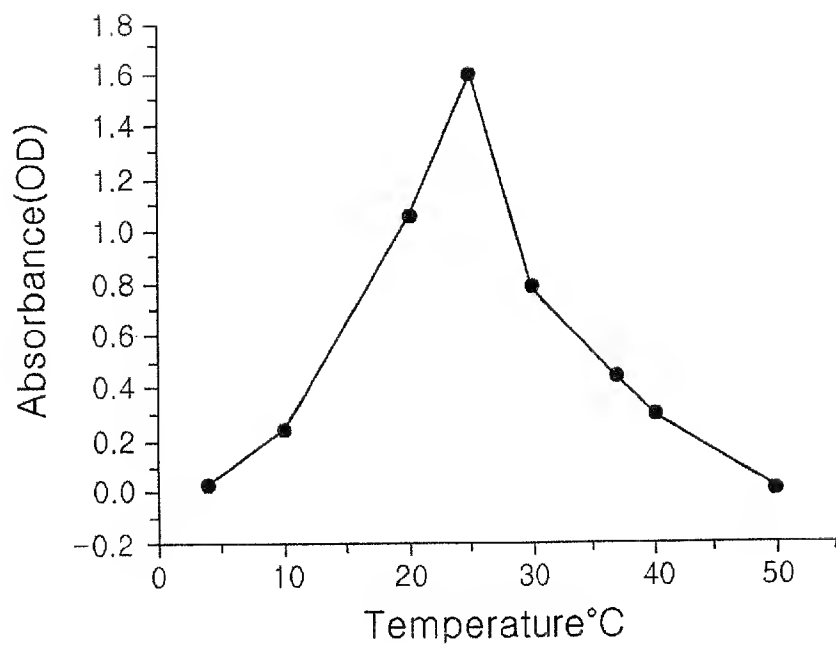


FIG. 3

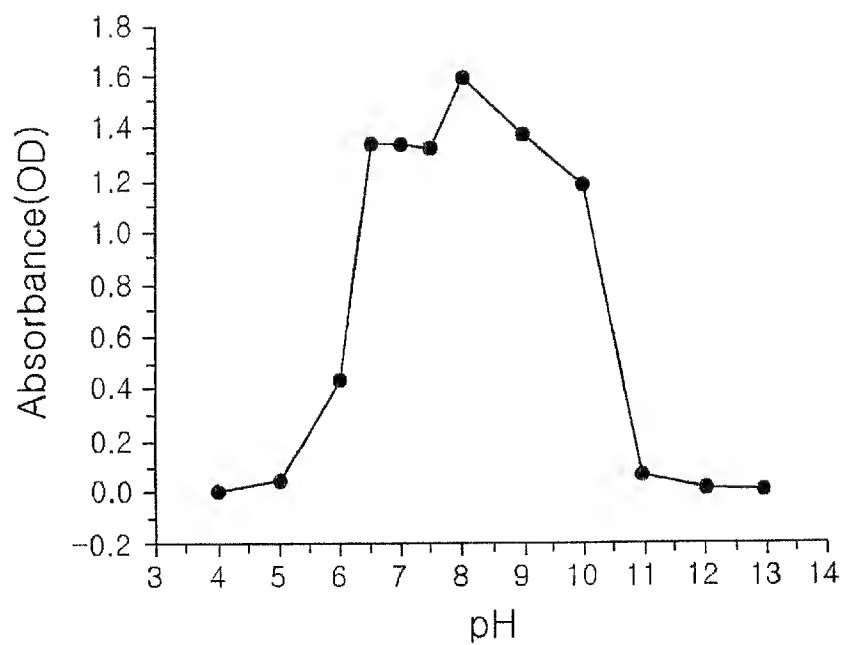
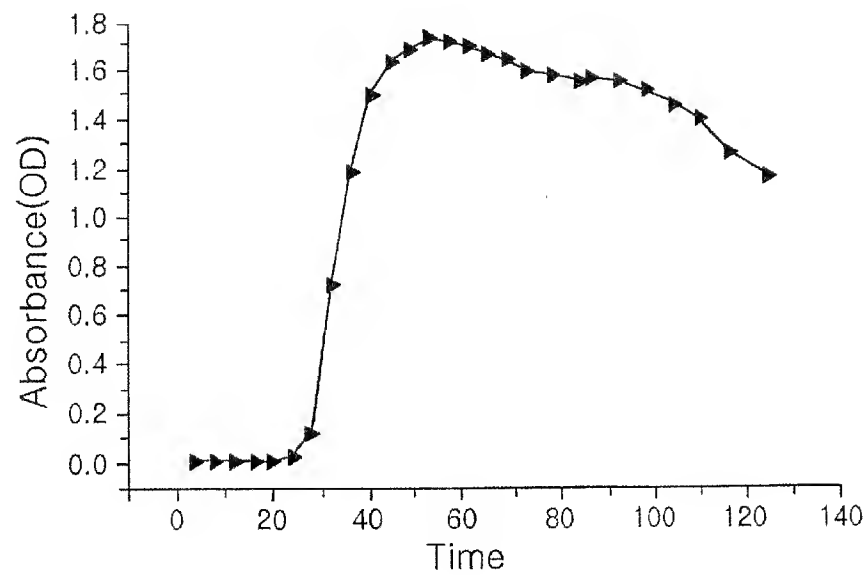


FIG. 4



**FIG. 5**

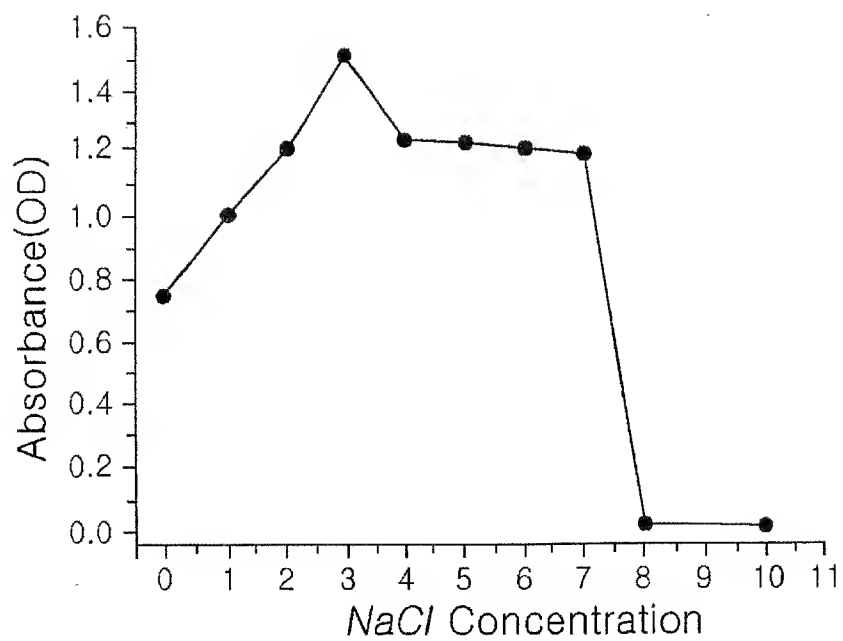


FIG. 6

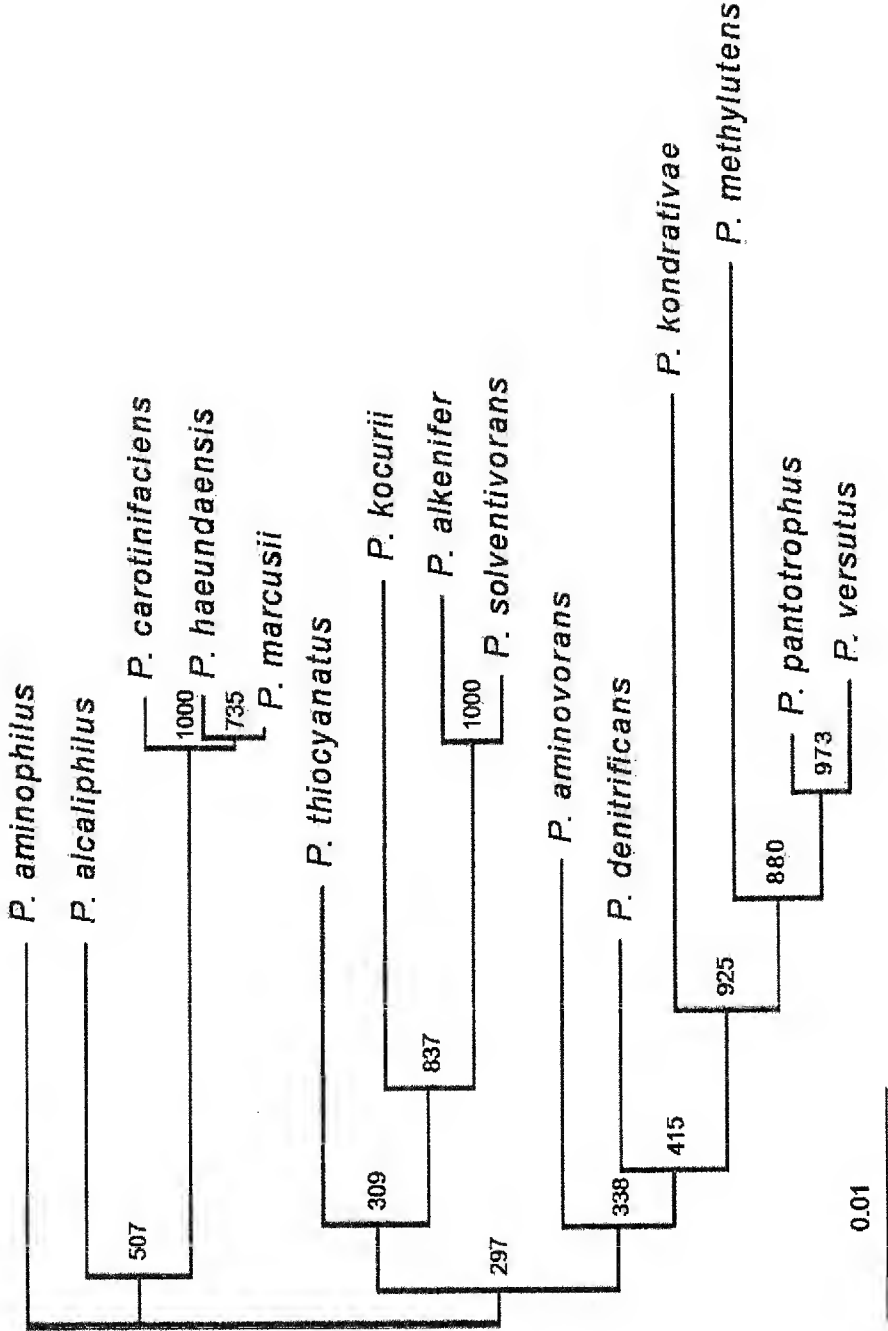


FIG. 7

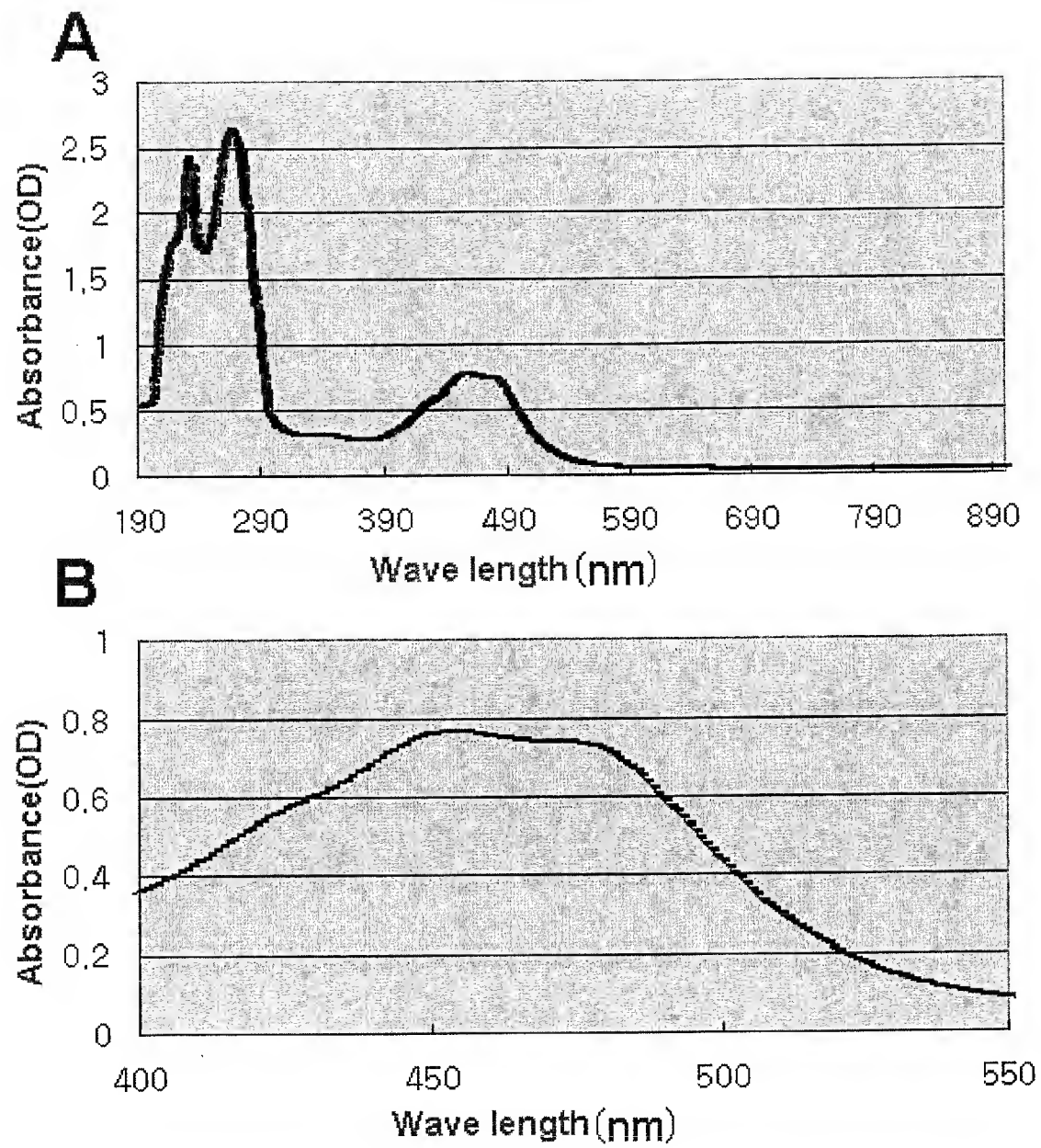


FIG. 8

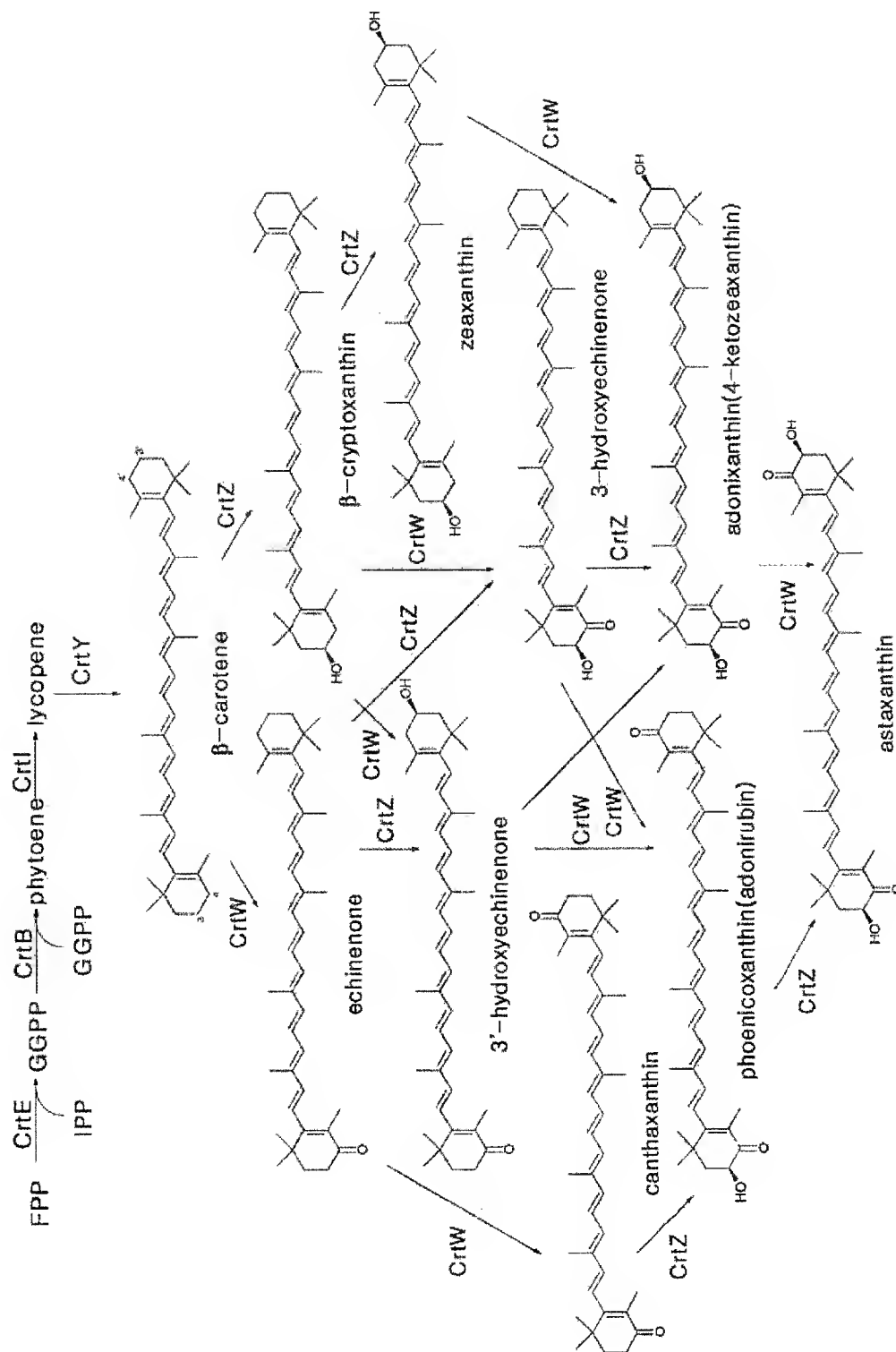




FIG. 9

	1	100
<i>P. haemdaesis</i>	(1) -----NSAHALPXADLIWLSIVSGGIIAANAHLHVAHWFLDAARPIIAIANFLGIL-WLSVGLFIANDAHGSSVFPGRPGNAWAGQLVW	
<i>Alcaligenes_sp</i>	(1) -----NSGRKPTTODTYNGLTAALLICWLYLHAFTLWLLDAARPELLAVCLAGLT-WLSVGLFIANDAHGSSVFPGRPRANAALGQLAW	
<i>Bradyrhizobium_sp</i>	(1) MHATAKATEFGASRRDDARQRYGLTAAVITAAWLYLVGLNFFWPLTLSLIPALPLVYLQWLYVGLFIANDCHGSSLVPPFPQVNRRI GQLCLF	
Consensus	(1) NSAKATVLSAALIAAWLYLHV LWFDAARPELLAIL LLSLT WLSVGLFIANDAHGSSVFPGRPRANAALGQL LW	
	101	200
<i>P. haemdaesis</i>	(90) LYAGESWRXNLYKHNHHRHGTGDDDDFEDHG---GPRNVAREIGTVFGWREGILLPIVTVVAILGD-RWNVYFVWPLPSILASIQLFVFGTWLPHR	
<i>Alcaligenes_sp</i>	(90) LYAGESWPXLIANKHTHRRAGTDNDFEDHG---GPRNVGSPFTYFGWREGILLPIVTVVAILGD-RWNVYFVWPLPSILASIQLFVFGTWLPHR	
<i>Bradyrhizobium_sp</i>	(101) LYAGESFDALNVEHKKHHPGTAEQDEVPFGFWHWFASFELHVFQWQVALIAVSLVYQIVFAPLQNLLEWALPGLLSALQLEFGTYLP HK	
Consensus	(101) LYAGESW KLIYKHN HRRH GTDDDDFEDHG GPRNVASFI TYFGWREGILLPIVTVVAILGD RWNVYFVWPLPSILASIQLFVFGTWLPHR	
	201	259
<i>P. haemdaesis</i>	(186) PGHDAEPDRHNAESSISDPVSLTCTHFGGYHNEHHLHPTVWWELESTRTKGDT A--	
<i>Alcaligenes_sp</i>	(186) PGHDDPDRHNAESTGIGDPLSLTCTHFGGYHNEHHLHPTVWWELESTRTKGDA--	
<i>Bradyrhizobium_sp</i>	(201) PATQPFADRHNAITSEPPANLSLTCTHFG-FHNEHHLHPTDAPWRLPEIKRBALERRD	
Consensus	(201) PGHD FPDHNAESS I DPLSLTCTHFGGYHNEHHLHPTVWWELESTRTKG A	

FIG. 10

	1	100
P. haemdaesis (1)	MTNELIYYAVLVNELTATSVRRNTNHCPLGCGNKHSHHEEDHAEKNDLYGCVFATATVFTVGNITQAPVLPWTALGNTVYGLTYFVHDSYQREN	
Alcaligenes_sp (1)	MTQELIYYAVLVNELTATSVRRNTNHCPLGCGNKHSHHEEDHAEKNDLYGCVFATATLFTVGNAYWPEVLPWTALGNTVYGLTYFTHDGLYQREN	
Consensus (1)	MTNELIYYAVLVNELTATSVRRNTNHCPLGCGNKHSHHEEDHAEKNDLYGCVFATATLFTVG V PVLWTALGNTVYGLTYFTHDGLYQREN	
	101	163
P. haemdaesis (101)	PERYTPRNGVARRLYQAHLHHAVEGRDHCVSFGFTYAPPVVKLQDLKTSGLRRAEQRT	
Alcaligenes_sp (101)	PERYTPRNGVARRLYQAHLHHAVEGRDHCVSFGFTYAPPVVKLQDLKTSGLRQDERPS	
Consensus (101)	PERYTPRNGY RRLYQAHLHHAVEGRDHCVSFGFTYAPPVVKLQDLK SGLR S	

FIG. 11

	1		100
P. haemdaesis	(1)	VT HDVLLAGAGL ANGELTALALBAEPMLRVLLDHAAGES DGH TNSCHPDLSPHLARLP LRAWNPQEVPEPHARLATGVSNDGHALADAYAR	
Flavobacterium_sp	(1)	NS HDLLIAGAGLSGHALIHLAVDRERDAKI VMLDASGSGDHT NSCHTDLSPWLARLSFIEGGWTFDQEVAFEDHSEKLTITGVSIEAGALIGLQ-	
Consensus	(1)	NS HDLLIAGAGL AALLALR EPD KILLD AGESD HTNSCHD DLSP WLARL PIRRA W DQEV FP HARL TGVSIDAAAL L	
	101		200
P. haemdaesis	(101)	SGAEIWNSDIALLDEQALISOSTRIEAGAVLDGGAQPSRLTVGFQKFGVKEIETDCPHGUPREHINDATVTTQDGTREIVLLFFSPTILLIEDTRY	
Flavobacterium_sp	(100)	-GVDLKWNTHVATLDDTGATLTDGSKRIEACVIDARGAVETPLTVGFQKFGVKEIETDAPHGVERPHINDATVPPQMDGTREIVLLFFSPTILLIEDTRY	
Consensus	(101)	G DIRVNS IA LDD GATLS GSRIEAA VIDARGA S HLTVGFQKFGVKEIETD PHGV REHINDATV Q DGTREIVLLFFSPTILLIEDTRY	
	201		300
P. haemdaesis	(201)	SDGSLDDDLAASDHVARQQWVGAEVBERGKILPIALAHDAAGFWADHAGPPVGLRAGGFHPVTGSLPYAAQVADVAGLSGPPGTDALEGAIR	
Flavobacterium_sp	(199)	SDGSLDDGALAQASLDYAAERGWTGQENBERGKILPIALAHDAIGFWRDHAGAVPVGLSAGLFFHPVTGSLPYAAQVADALAA--DLTASARRAVE	
Consensus	(201)	SDGSLDD ALA AS DYA GWTG ENBERGKILPIALAHDA GEW DHA G VPVGL AG FHPVTGSLPYAAQVAD IAA T A R AIR	
	301		387
P. haemdaesis	(301)	DYALDRARDRFLELLNMLFERGAPDRDYTLLOQFVBNPHGLIERFTAGLSVAHQALVTGKPIELGTAIRCLPERILLKENA	
Flavobacterium_sp	(297)	GWALDRARDRFLELLNMLFERGAPDRDYTLLOQFVBNPHGLIERFTAGLTLADRLVTGKPIELSGAVCLPERILLQERA	
Consensus	(301)	WALDRA RDRFLELLNMLFERG PDRY LLQRFYRLP LIERFTAGLSLAD LKIVTKKPIPL AIRCLPERILL E A	

FIG. 12

	1	100
P. haeundaesis	(1)	MNAHSPAAKT XI VI GAGF GGLALAI RLQSAGI AT TLVEARDK PGRAYVYVNDQGHVEDAGT VI TDDALKE LWA L TGODNARDVT LMPVSPFFYELNMPG
Flavobacterium_sp	(1)	-----HSSAT VI GAGF GGLALAI RLQSAGI AT TLVEARDK PGRAYVYVNDQGHVEDAGT VYTDPSLEELWALSGOPHEEDVT LIPVSPFFYELT WAD
Consensus	(1)	S I VI GAGF GGLALAI RLQSAGI AT TLVEARDK PGRAYVYVNDQGHVEDAGT VI TDDALKE LWA LSGQ M EDVT LIPVSPFFYEL W
	101	200
P. haeundaesis	(101)	GKVEDYVNEADQLE RQIAQFNE DDEGTVRRERYAAEYVYQGVYKLGTVFELKLGQMLKAPALMKLEAYKSHAKVATFIKDPYLRQAFSEYHTLLVGN
Flavobacterium_sp	(94)	GRSEFYVNDDELLRQVASFWEADVDGYRREFHDYAAEYVREGYVYKLGTTPELKLQQLNMAAPALMRLLQAYESVHSHVAREFIQDPHLRQAFSEHTLLVGN
Consensus	(101)	GKFDYVND D L RQIA FNP DLDGYRRE DYAEVY EGYVYKLGTVFELKLQQL AAPALMKL AYKSVHA VA FI DPHLRQAFSEHTLLVGN
	201	300
P. haeundaesis	(201)	PESTSIYALIHALERGGYWEAKGGTNQLVAGNVALFERLGGQNMNAKVARLETGARTTGVTLADGRSLEADWVASNGDVHNVYEDLLIGHTAEGQSR
Flavobacterium_sp	(194)	PESTSIYALIHALERGGYWEAKGGTNQLVAGNVALFERLGGTLLINARTRIDTEGDEATGVTLIGRQLRATVASNGDVHNSYEDLLIGHTRGRYK
Consensus	(201)	PESTSIYALIHALERGGYWEAKGGTNQLVAGNVALFERLGG LLINAKV RIDTEG R TGVTL DGR LRAD VASNGDVNH YEDLLIGHT RG SK
	301	400
P. haeundaesis	(301)	AKSLDKRWSLEVLHFGLEHAPMDIAHHTILFQPRYRELVNEIFKGPKEADESLYLHSPCTTDDMAPPGMSTHYVLAPVPHLGRÆIDWAVEGPBY
Flavobacterium_sp	(294)	AAILNKRWSLEVLHFGLSRPERNLAHSHVIEGPRYKGLVNEIFNRPRLPDDSNYLHSPCTDPSLAPGNMSTHYVLAPVPHLGRADVDWEAEAPGY
Consensus	(301)	A L R RWSWSLEVLHFG L P IAHSLIEGPYK LYNEIF GPKL DDESLYLHSPC TDP LAP GMSTHYVLAPVPHLGRADIDW EAP Y
	401	500
P. haeundaesis	(401)	ADRI LASEELIPNLKAMLTTRITPADFASELNAHGSÆSVEPILTQS AWEPRHMDKTIENFYIVGAGTHPGAGIPGVVGS AKAT AQVWLSDLAG
Flavobacterium_sp	(394)	AERIPEELEREATPDLRKHLTYSEIFSPÆSTELS AHHGSÆSVEPILTQS AWEPRHMDRAIPNFYIVGAGTHPGAGIPGVVGS AKAT AQVWLSDLAV
Consensus	(401)	ADRI LE R IP LR LT SRIESPADFAS EL AHHGSÆSVEPILTQS AWEPRHMDK I NFYIVGAGTHPGAGIPGVVGS AKAT AQVWLSDLA
	501	
P. haeundaesis	(501)	A

FIG. 13

	1	100
P. haendaesis	(1)	MSDEVLTSTEAITQSGQSEAT AAKLNEFCIEDDTVNL YAWCEHDDVIDQALSSREAVNDPQALDGLRVTI AALQDGPVTPPEAALRAVARRHDF
Flavobacterium_sp	(1)	MTDLTATSEAAIAGSGSQFQAQAKLNPPEGEIEDTVNYAWCEHDDVIDQVNGSAPEAGGPPQARLIGALRADTIALMHEGNSPFFAALLQVARRHDF
Consensus	(1)	MSDL TS AI QGSGQFA AAKLNPPEGEIEDTVNYAWCEHDDVIDSQ LGS PEA DPQARL ALB DTLAAL DGPNSPFAALR VARRHDF
	101	200
P. haendaesis	(101)	PQAWPNDLIEGFANDVEADRYETLDVLEYSYHYAGTVGVMARVNGVEDPVLDRACDLGLAFQLTNIARDYIDDARIQECYLPGLDQKARLDAPV
Flavobacterium_sp	(101)	PDLNPNDLIEGFANDVADREYESLDVLEYSYHYAGTVGVMARVNGVQDDAFLDRACDLGLAFQLTNIARDYIDDARIQECYLPADFLAEGATVEGEP
Consensus	(101)	P WPNDLIEGFANDV RDEYSLDVLEYSYHYAGTVGVMARVNGV DD VLDRACDLGLAFQLTNIARDYIDDA IGRCYLPADUL AGA IDGPV
	201	300
P. haendaesis	(201)	PSPELYTVILELLDEAPYYASARVGLADLPDPCAWSTAAALRIYRALTEIENSGPQVYRQEI STSTAATIGLGVGGDVARSKLPAGVSRQGLWTR
Flavobacterium_sp	(201)	PSDALYSVTIRLLDAEPYYASARGLPPLDPCAWSTAAALRIYRALTEIENSGPQVYRQEI STSTAATIGLARGHLDAAHSRLRGGEISDGLWTR
Consensus	(201)	PS LYSVTIRLLD AEPYYASAR GL LPPRCANSTAAALRIYRAG RIR GP AYRQRLSTAAKLGLLA GG D A SRL GA ISR GLWTR
	301	
P. haendaesis	(301)	PHHV
Flavobacterium_sp	(301)	PRA-
Consensus	(301)	P

FIG. 14

	1	100
P. haemdaesis	(1)	NRDYPITAIILQRIEETAQTEAVSQIGRANSHGLSSRRERCHMLLAFAAGVQOTIYDACAVENTHAASLIFFDLPCNDACLRGEPAT
Flavobacterium_sp	(1)	WPKQPPRLVEIRLQISQPGVYSRLGAAHNDALSPGEPFVNLNWHSSGTVCAWVDAACAVENVHAASLIFDINCHDARTKGPAT
Consensus	(1)	N N LL BL IA EG VS PIGAAH ALS GREFRANMLL AEGSGVCD IYDACAVENTHAASLIFDILPCNDAA RRG PAT
	101	200
P. haemdaesis	(101)	HYAHGSRATLGGLALITETAHALLAGARGSGTVPAQLVRLISLSPQGLCAGQDLDLHAANGHGTVEQEQLMTGVLEPTAGLENLAVIKETPAEEQTQ
Flavobacterium_sp	(101)	HYAHGGRATLALITETANLLGEHGTPTDQAPRLVASHNRANQFVGLCAGQDLDLHAPYDAGTEREDMTGVLEPTAGLENLSIIGLQNKETEQ
Consensus	(101)	HYAHGCE BAYIAGTALITETAN ILLA ARGAS RA LY LSRALGP GICGAGQDLDLHA K HAGLE EQDLKTVLEPTAGLENLAIK D E Q
	201	295
P. haemdaesis	(201)	MTDFGRQLGRTVQSVDLLDVQDQALGKDTGRDAAPPRKGLAYSQIQNVSHVTEACAGLJAHLSKNIQAPETALLENVDPYAHAA--
Flavobacterium_sp	(201)	LNARGRQLGRTVQSVDLLDVTDVASTGDTATATAPGPGGLNAGQGDYAGHYEASRAGDELNETLEFGGQIADLLANIPHTIRKSA
Consensus	(201)	LI FGRQLGRTVQSVDLLDVTD AA GKTARD AAGPYN GLLAY L YA HY ASRAOLD LLRSK A IA LL RYLPB B

FIG. 15

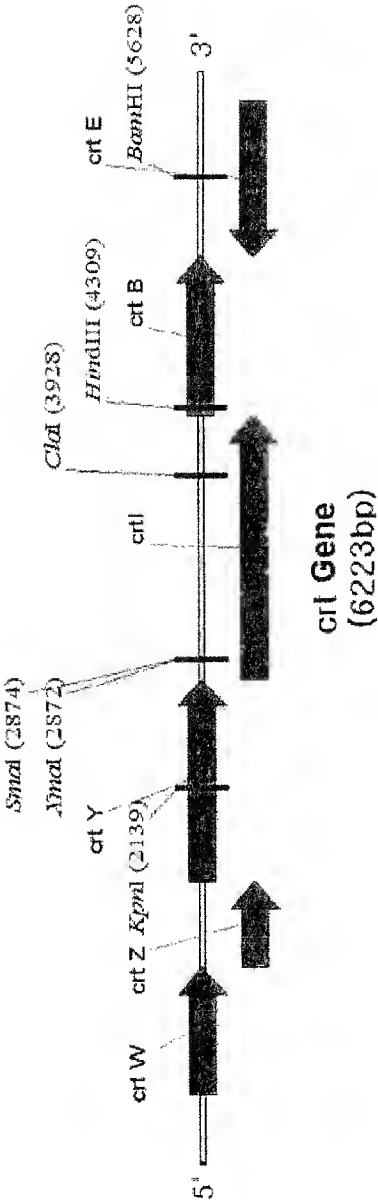


FIG. 16

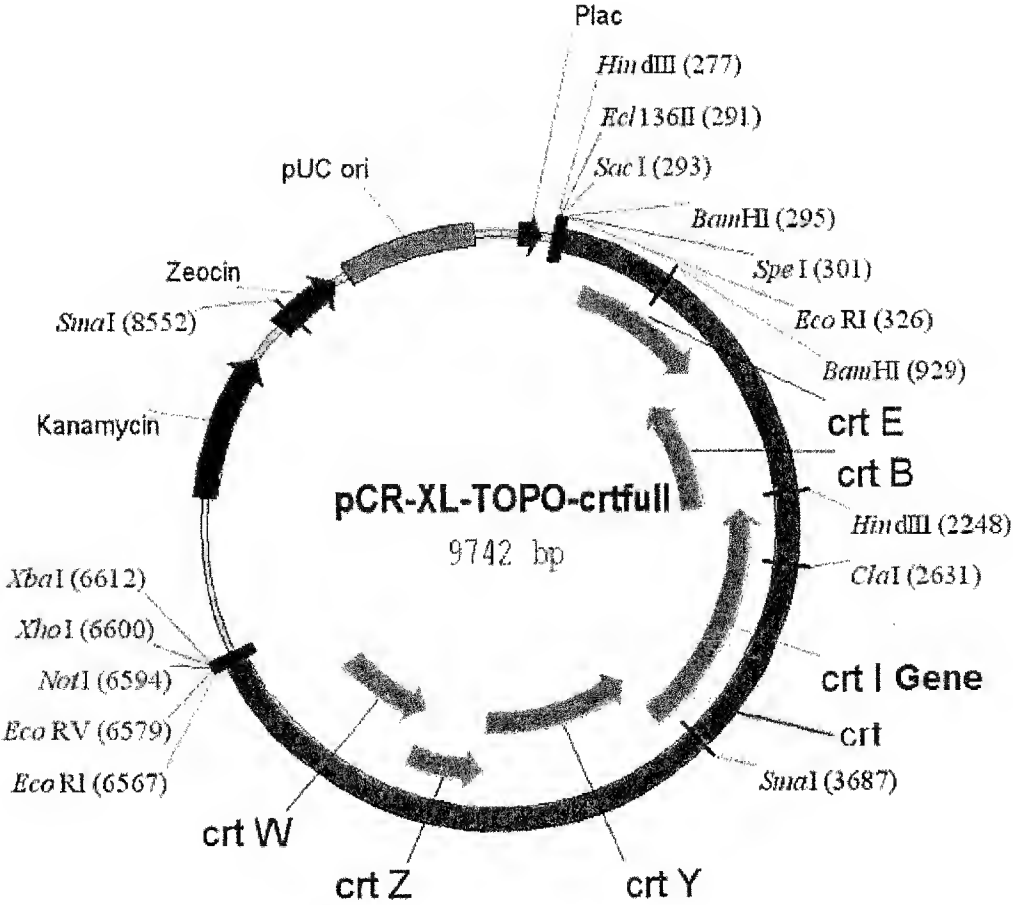




FIG. 17

